

F. Kounelis, A. Kanavos, I.E. Livieris, G. Vonitsanos and P. Pintelas. [Predicting secondary structure for human proteins based on Chou-Fasman method](#)

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**Abstract** - Proteins are constructed by the combination of a different number of amino acids and thus, have a different structure and folding depending on chemical reactions and other aspects. The protein folding prediction can help in many healthcare scenarios to foretell and prevent diseases. The different elements that form a protein give the secondary structure. One of the most common algorithms used for secondary structure prediction constitutes the Chou-Fasman method. This technique divides and in following analyses each amino acid in three different elements, which are  $\alpha$ -helices,  $\beta$ -sheets and turns based on already known protein structures. Its aim is to predict the probability for which each of these elements will be formed. In this paper, we have used Chou-Fasman algorithm for extracting the probabilities of a series of amino acids in FASTA format. We make an analysis given all probabilities for any length of a human protein without any restriction as other existing tools.